GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 05:33:11 ; Search time 3376 Seconds
(without alignments)
16482.395 Million cell updates/sec

Title: US-09-589-510-3
Perfect score: 1912
Sequence: 1 acccacgcgtccgcaaattt.....aaaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 100

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1912	100.0	1912	6	AX077226	AX077226 Sequence
2	1080	56.5	1869	6	AX077232	AX077232 Sequence
3	576	30.1	1845	6	AX077224	AX077224 Sequence

ALIGNMENTS

RESULT 1
AX077226
LOCUS AX077226 1912 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 3 from Patent WO0105975.
ACCESSION AX077226
VERSION AX077226.1 GI:13121820
KEYWORDS .
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1912)
AUTHORS Mahajan,P.B.
TITLE Maize orthologues of bacterial ruvb:cdnas and uses thereof
JOURNAL Patent: WO 0105975-A 3 25-JAN-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  Sequence 9 from Patent WO0105975.
ACCESSION   AX077232
VERSION     AX077232.1  GI:13121826
KEYWORDS    .
SOURCE      Zea mays.
  ORGANISM  Zea mays
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1869)
  AUTHORS   Mahajan,P.B.
  TITLE     Maize orthologues of bacterial ruvb:cdnas and uses thereof
  JOURNAL   Patent: WO 0105975-A 9 25-JAN-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
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RESULT 3
AX077224
LOCUS       AX077224               1845 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 1 from Patent WO0105975.
ACCESSION   AX077224
VERSION     AX077224.1  GI:13121818
KEYWORDS    .
SOURCE      Zea mays.
  ORGANISM  Zea mays
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            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1845)
  AUTHORS   Mahajan,P.B.
  TITLE     Maize orthologues of bacterial ruvb:cdnas and uses thereof
  JOURNAL   Patent: WO 0105975-A 1 25-JAN-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
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  Query Match           30.1%;  Score 576;  DB 6;  Length 1845;
  Best Local Similarity  98.8%;  Pred. No. 0;
  Matches 1426;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      84 GTTGGCGGCGATGAGGATCGAGGAGGTGCAGTCGACCTCGAAGAAGCAGCGCATCGCCAC 143
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75 GTTGGCGGCGATGAGGATCGAGGAGGTGCAGTCGACCTCGAAGAAGCAGCGCATCGCCAC 134

Qy     144 CCACACCCACATCAAGGGACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGC 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     135 CCACACCCACATCAAGGGACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGC 194

Qy     204 GGGGTTCGTGGGCCAGGCGGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCG 263
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     195 GGGGTTCGTGGGCCAGTCGGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCG 254

Qy     264 CCAGAAGAAGATGGCCGGCCGCGCGGTGCTCCTTGCGGGTCCGCCCGCCACGGGCAAGAC 323
           |||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     255 CCAGAAAAAGATGGCCGGCCGCGCGGTGCTCCTTGTGGGTCCGCCCGCCACGGGCAAGAC 314

Qy     324 GGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGTCCTATGGT 383
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
```

```
Db    315 GGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGCCCTATGGT 374

Qy    384 AGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCG 443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 AGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCG 434

Qy    444 TAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGA 503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 TAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGA 494

Qy    504 ACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTAGCCATGT 563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 ACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTAGCCATGT 554

Qy    564 AATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTA 623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 AATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTA 614

Qy    624 TGATGCTCTGATCAAGGAAAAGGTGGCAGTGGGTGATGTTATATACATCGAAGCAAATAG 683
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    615 TGATGCTCTGATCAAGGAAAAGGTGGCAGTGGGTGATGTTATATACATTGAAGCAAATAG 674

Qy    684 TGGAGCAGTGAAAAGAGTTGGTAGATGTGATTCTTTTGCTACAGAATACGATCTTGAAGC 743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 TGGAGCAGTGAAAAGAGTTGGTAGATGTGATTCTTTTGCTACAGAATACGATCTTGAAGC 734

Qy    744 TGAAGAGTATGTTCCTATCCCCAAAGGTGAAGTCCATAAGAAAAAAGAAATTGTGCAGGA 803
          |||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    735 TGAAGAATATGTTCCTATCCCCAAAGGTGAAGTCCATAAGAAAAAAGAAATAGTGCAGGA 794

Qy    804 TGTCACACTTCATGACCTTGATGCAGCAAATGCTCAGCCACAAGGTGGCCAAGATATTTT 863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    795 TGTCACACTTCATGACCTTGATGCAGCAAATGCTCAGCCACAAGGTGGCCAAGATATTTT 854

Qy    864 GTCCCTTATGGGCCAGATGATGAAACCACGAAAGACTGAAATCACCGAAAAACTACGCCA 923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    855 GTCCCTTATGGGCCAGATGATGAAACCACGAAAGACTGAAATCACCGAAAAACTACGCCA 914

Qy    924 AGAAATTAATAAGGTGGTAAATAGATATATCGATGAAGGAATTGCAGAGCTTGTACCTGG 983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    915 AGAAATTAATAAGGTGGTAAATAGATATATCGATGAAGGAATTGCAGAGCTTGTACCTGG 974

Qy    984 TGTTTTGTTCATTGATGAGGTCCACATGTTGGATATCGAATGTTTTTCTTATCTTAACCG 1043
          |||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    975 TGTTTTATTCATTGACGAGGTCCACATGTTGGATATCGAATGTTTTTCTTATCTTAACCG 1034

Qy   1044 TGCATTGGAGAGCCCATTATCACCAATCGTGATACTTGCTACAAATAGGGGAATATGTAA 1103
          |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Db   1035 TGCATTGGAGAGCCCATTATCACCAATTGTGATACTTGCTACGAATAGGGGAATATGTAA 1094

Qy   1104 TGTAAGAGGAACTGATATGACAAGTCCACATGGTATACCGGTGGATCTTCTAGATAGGCT 1163
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||| |
Db   1095 TGTAAGAGGAACTGATATGACAAGTCCACATGGTATACCAGTGGATCTTCTAGATAGGTT 1154

Qy   1164 GGTGATTATTCGGACAGAGACATATGGCCCTACTGAGATGATACAGATATTGGCTATCCG 1223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1155 GGTGATTATTCGGACAGAGACATATGGCCCTACTGAGATGATACAGATATTGGCTATCCG 1214

Qy   1224 AGCACAAGTGGAGGAGATTGATATGGATGAAGAAAGTCTTGCTTATTTAGGCGAGATCGG 1283
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1215 AGCACAAGTGGAGGACATTGATATGGATGAAGAAAGTCTTGCTTATTTAGGCGAGATCGG 1274

Qy   1284 ACAGCAGACATCTTTGAGACATGCTATTCAATTGATATCACCTGCCAGCGTGGTCTCAAA 1343
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1275 ACAGCAGACATCTTTAAGACATGCTATTCAATTGATATCACCTGCCAGCGTGGTCTCAAA 1334

Qy   1344 GACTAATGGAAGAGAGAAAATCTGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTT 1403
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1335 GACTAATGGAAGAGAGAAAATATGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTT 1394

Qy   1404 GGATGCCAAATCCTCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGAT 1463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1395 GGATGCCAAATCCTCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGAT 1454

Qy   1464 TTGGATCTCCTGTCGTGGAAGTCTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTA 1523
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1455 TTGGATCACCTGTCGTGGAAGTCTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTA 1514

Qy   1524 GTG 1526
          |||
Db   1515 GTG 1517
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Search completed: December 5, 2002, 07:18:13
Job time : 3390 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 06:14:52 ; Search time 2048 Seconds
(without alignments)
15120.005 Million cell updates/sec

Title: US-09-589-510-3
Perfect score: 1912
Sequence: 1 acccacgcgtccgcaaattt.....aaaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 100

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	510	26.7	612	14	BM736448	BM736448 952050H12
	2	403	21.1	610	10	BE512278	BE512278 946066D09
	3	318	16.6	1542	11	AY109398	AY109398 Zea mays
	4	298	15.6	474	10	BE512426	BE512426 946071A06
	5	248	13.0	248	10	BE512215	BE512215 946066A01
c	6	134	7.0	549	10	BE512425	BE512425 946071A06
c	7	113	5.9	318	14	BM736925	BM736925 952050H12
c	8	110	5.8	375	10	BE640273	BE640273 946082B06
c	9	109	5.7	109	12	BG316941	BG316941 947024C05

ALIGNMENTS

RESULT 1
BM736448
LOCUS BM736448 612 bp mRNA linear EST 01-MAR-2002
DEFINITION 952050H12.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.
ACCESSION BM736448
VERSION BM736448.1 GI:19057781
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 612)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952050 row: H column: 12.
FEATURES Location/Qualifiers
source 1..612
/organism="Zea mays"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
/tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth phases"
/lab_host="DH10B"
/note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."
BASE COUNT 159 a 143 c 199 g 111 t
ORIGIN

Query Match 26.7%; Score 510; DB 14; Length 612;
Best Local Similarity 99.7%; Pred. No. 6.4e-122;
Matches 610; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      42 AGGAGGCAGCTCCACAGAAACAGAGAGCGCATAACCGGCGGCGTTGGCGGCGATGAGGAT 101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGGAGGCAGCTCCACAGAAACAGAGAGCGCATAACCGGCGGCGTTGGCGGCGATGAGGAT 60

Qy     102 CGAGGAGGTGCAGTCGACCTCGAAGAAGCAGCGCATCGCCACCCACACCCACATCAAGGG 161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGAGGAGGTGCAGTCGACCTCGAAGAAGCAGCGCATCGCCACCCACACCCACATCAAGGG 120

Qy     162 ACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGCGGGGTTCGTGGGCCAGGC 221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGCGGGGTTCGTGGGCCAGGC 180
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Qy     222 GGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCGCCAGAAGAAGATGGCCGG 281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCGCCAGAAGAAGATGGCCGG 240

Qy     282 CCGCGCGGTGCTCCTTGCGGGTCCGCCCGCCACGGGCAAGACGGCGCTAGCGCTCGGCAT 341
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCGCGCGGTGCTCCTTGCGGGTCCGCCCGCCACGGGCAAGACGGCGCTAGCGCTCGGCAT 300

Qy     342 AGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGTCCTATGGTAGGATCAGAAGTGTACTC 401
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGTCCTATGGTAGGATCAGAAGTGTACTC 360

Qy     402 CTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCGTAGAGCTATAGGTTTGCG 461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCGTAGAGCTATAGGTTTGCG 420

Qy     462 TATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGAGGC 521
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGAGGC 480

Qy     522 TGAGAGTACAACTGGTGGATATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAAGAC 581
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TGAGAGTACAACTAGTGGATATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAAGAC 540

Qy     582 TGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATCAAGGA 641
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGGTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATCAAGGA 600

Qy -   642 AAAGGTGGCAGT 653
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Db     601 AAAGGTGGCAGT 612
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RESULT 2
BE512278

LOCUS	BE512278	610 bp	mRNA	linear	EST 07-AUG-2000

DEFINITION 946066D09.y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION BE512278
VERSION BE512278.1 GI:9733421
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 610)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946066 row: D column: 09.

FEATURES Location/Qualifiers
source 1. .610
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassel primordium prepared by Schmidt lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to inflorescence development"
/lab_host="XLOLR"
/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

BASE COUNT 160 a 135 c 196 g 119 t
ORIGIN

Query Match 21.1%; Score 403; DB 10; Length 610;
Best Local Similarity 99.5%; Pred. No. 1.8e-94;
Matches 553; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy     116 CGACCTCGAAGAAGCAGCGCATCGCCACCCACACCCACATCAAGGGACTCGGCCTCGACG 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31 CGACCTCGAAGAAGCAGCGCATCGCCACCCACACCCACATCAAGGGACTCGGCCTCGACG 90

Qy     176 CCAATGGGATGGCGATTGCGTTGGCGGCGGGGTTCGTGGGCCAGGCGGCGGCGCGCGAGG 235
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      91 CCAATGGGATGGCGATTGCGTTGGCGGCGGGGTTCGTGGGCCAGTCGGCGGCGCGCGAGG 150

Qy     236 CGGCCGGGCTGGCGGTCGACATGATTCGCCAGAAGAAGATGGCCGGCCGCGCGGTGCTCC 295
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     151 CGGCCGGGCTGGCGGTCGACATGATTCGCCAGAAAAAGATGGCCGGCCGCGCGGTGCTCC 210

Qy     296 TTGCGGGTCCGCCCGCCACGGGCAAGACGGCGCTAGCGCTCGGCATAGCCCAGGAGCTCG 355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 TTGCGGGTCCGCCCGCCACGGGCAAGACGGCGCTAGCGCTCGGCATAGCCCAGGAGCTCG 270

Qy     356 GCAGCAAGGTCCCTTTCTGTCCTATGGTAGGATCAGAAGTGTACTCCTCGGAGGTCAAGA 415
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     271 GCAGCAAGGTCCCTTTCTGCCCTATGGTAGGATCAGAAGTGTACTCCTCGGAGGTCAAGA 330

Qy     416 AAACTGAGGTGCTGATGGAAAATTTCCGTAGAGCTATAGGTTTGCGTATAAAGGAAAACA 475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     331 AAACTGAGGTGCTGATGGAAAATTTCCGTAGAGCTATAGGTTTGCGTATAAAGGAAAACA 390

Qy     476 AAGAGGTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGAGGCTGAGAGTACAACTG 535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 AAGAGGTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGAGGCTGAGAGTACAACTG 450

Qy     536 GTGGATATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAAGACTGTTAAAGGGACTA 595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451 GTGGATATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAAGACTGTTAAAGGGACTA 510

Qy     596 AGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATCAAGGAAAAGGTGGCAGTGG 655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 AGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATCAAGGAAAAGGTGGCAGTGG 570

Qy     656 GTGATGTTATATACAT 671
           ||||||||||||||||
Db     571 GTGATGTTATATACAT 586
```

RESULT 3
AY109398

LOCUS	AY109398	1542 bp	mRNA	linear	HTC 25-MAY-2002

DEFINITION Zea mays CL5641_1 mRNA sequence.
ACCESSION AY109398
VERSION AY109398.1 GI:21213108
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1542)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1542)
AUTHORS Coe,E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of

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          Missouri, Columbia, MO 65211, USA
FEATURES             Location/Qualifiers
     source          1. .1542
                     /organism="Zea mays"
                     /db_xref="MaizeDB:632456"
                     /db_xref="taxon:4577"
                     /clone="CL5641_1"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
BASE COUNT      386 a    318 c    397 g    347 t     94 others
ORIGIN

  Query Match             16.6%;  Score 318;  DB 11;  Length 1542;
  Best Local Similarity   99.5%;  Pred. No. 5e-73;
  Matches  418;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     252 CGACATGATTCGCCAGAAGAAGATGGCCGGCCGCGCGGTGCTCCTTGCGGGTCCGCCCGC 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 CGACATGATTCGCCAGAAGAAGATGGCCGGCCGCGCGGTGCTCCTTGCGGGTCCGCCCGC 280

Qy     312 CACGGGCAAGACGGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTT 371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     281 CACGGGCAAGACGGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTT 340

Qy     372 CTGTCCTATGGTAGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGAT 431
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     341 CTGCCCTATGGTAGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGAT 400

Qy     432 GGAAAATTTCCGTAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGG 491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     401 GGAAAATTTCCGTAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGG 460

Qy     492 AGAGGTTACTGAACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGATATGCAAAAAG 551
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     461 AGAGGTTACTGAACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGATATGCGAAAAG 520

Qy     552 CATTAGCCATGTAATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAACTGAAGTTAGA 611
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     521 CATTAGCCATGTAATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAACTGAAGTTAGA 580

Qy     612 TTCTTCAATTTATGATGCTCTGATCAAGGAAAAGGTGGCAGTGGGTGATGTTATATACAT 671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     581 TTCTTCAATTTATGATGCTCTGATCAAGGAAAAGGTGGCAGTGGGTGATGTTATATACAT 640


RESULT 4
BE512426
LOCUS       BE512426                 474 bp    mRNA    linear   EST 07-AUG-2000
DEFINITION  946071A06.y1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE512426
VERSION     BE512426.1  GI:9733674
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946071  row: A  column: 06.
FEATURES             Location/Qualifiers
     source          1. .474
                     /organism="Zea mays"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
BASE COUNT      110 a    121 c    162 g     81 t
ORIGIN

  Query Match             15.6%;  Score 298;  DB 10;  Length 474;
  Best Local Similarity   99.3%;  Pred. No. 2e-67;
  Matches  448;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      84 GTTGGCGGCGATGAGGATCGAGGAGGTGCAGTCGACCTCGAAGAAGCAGCGCATCGCCAC 143
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24 GTTGGCGGCGATGAGGATCGAGGAGGTGCAGTCGACCTCGAAGAAGCAGCGCATCGCCAC 83

Qy     144 CCACACCCACATCAAGGGACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGC 203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      84 CCACACCCACATCAAGGGACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGC 143

Qy     204 GGGGTTCGTGGGCCAGGCGGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCG 263
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     144 GGGGTTCGTGGGCCAGTCGGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCG 203

Qy     264 CCAGAAGAAGATGGCCGGCCGCGCGGTGCTCCTTGCGGGTCCGCCCGCCACGGGCAAGAC 323
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     204 CCAGAAAAAGATGGCCGGCCGCGCGGTGCTCCTTGCGGGTCCGCCCGCCACGGGCAAGAC 263

Qy     324 GGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGTCCTATGGT 383
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     264 GGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGCCCTATGGT 323

Qy     384 AGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCG 443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     324 AGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCG 383

Qy     444 TAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGA 503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     384 TAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGA 443

Qy     504 ACTTTCCCCAGAAGAGGCTGAGAGTACAACT 534
           |||||||||||||||||||||||||||||||
Db     444 ACTTTCCCCAGAAGAGGCTGAGAGTACAACT 474


RESULT 5
BE512215
LOCUS       BE512215                 248 bp    mRNA    linear   EST 07-AUG-2000
DEFINITION  946066A01.y1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE512215
VERSION     BE512215.1  GI:9733358
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
```

```
REFERENCE   1  (bases 1 to 248)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946066  row: A  column: 01.
FEATURES             Location/Qualifiers
     source          1. .248
                     /organism="Zea mays"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
BASE COUNT       87 a     37 c     63 g     61 t
ORIGIN

  Query Match             13.0%;  Score 248;  DB 10;  Length 248;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-54;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     399 CTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCGTAGAGCTATAGGTTT 458
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCGTAGAGCTATAGGTTT 60

Qy     459 GCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGA 518
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGA 120

Qy     519 GGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAA 578
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db .   121 GGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAA 180

Qy     579 GACTGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATCAA 638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GACTGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATCAA 240

Qy     639 GGAAAAGG 646
           ||||||||
Db     241 GGAAAAGG 248


RESULT 6
BE512425/c
LOCUS       BE512425                549 bp    mRNA    linear   EST 07-AUG-2000
DEFINITION  946071A06.x1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE512425
VERSION     BE512425.1  GI:9733673
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 549)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946071  row: A  column: 06.
FEATURES             Location/Qualifiers
     source          1. .549
                     /organism="Zea mays"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
BASE COUNT      150 a    146 c    116 g    137 t
ORIGIN

  Query Match             7.0%;  Score 134;  DB 10;  Length 549;
  Best Local Similarity   99.0%;  Pred. No. 2.2e-25;
  Matches  284;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    1240 ATTGATATGGATGAAGAAAGTCTTGCTTATTTAGGCGAGATCGGACAGCAGACATCTTTG 1299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     519 ATTGATATGGATGAAGAAAGTCTTGCTTATTTAGGCGAGATCGGACAGCAGACATCTTTA 460

Qy    1300 AGACATGCTATTCAATTGATATCACCTGCCAGCGTGGTCTCAAAGACTAATGGAAGAGAG 1359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     459 AGACATGCTATTCAATTGATATCACCTGCCAGCGTGGTCTCAAAGACTAATGGAAGAGAG 400

Qy    1360 AAAATCTGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTTGGATGCCAAATCCTCG 1419
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     399 AAAATATGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTTGGATGCCAAATCCTCG 340

Qy    1420 GCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTTGGATCTCCTGTCGT 1479
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     339 GCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTTGGATCACCTGTCGT 280

Qy    1480 GGAAGTCTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTAGTG 1526
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     279 GGAAGTCTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTAGTG 233


RESULT 7
BM736925/c
LOCUS       BM736925                318 bp    mRNA    linear   EST 01-MAR-2002
DEFINITION  952050H12.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
            mays cDNA, mRNA sequence.
ACCESSION   BM736925
VERSION     BM736925.1  GI:19058258
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 318)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
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            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 952050  row: H  column: 12.
FEATURES              Location/Qualifiers
     source           1. .318
                      /organism="Zea mays"
                      /cultivar="BMS (Black Mexican Sweet)"
                      /db_xref="taxon:4577"
                      /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA
                      )"
                      /tissue_type="suspension culture"
                      /dev_stage="mixed logarithmic and stationary growth
                      phases"
                      /lab_host="DH10B"
                      /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The
                      library was prepared by George Rudenko using poly (A)
                      selected RNA and Universal Riboclone cDNA Synthesis System
                      (Promega). cDNA was synthesized using both random and
                      oligo(dT) primers in separate reactions and equipped with
                      EcoRI adaptors. Library was size-fractionated on agarose
                      gels (for insert size >400bp) and non-directionally cloned
                      into EcoRI-digested pUC19 vector. Blue/white selection on
                      carbenicillin-containing plates was used to recover
                      positive clones."
BASE COUNT       86 a     78 c     62 g     92 t
ORIGIN

  Query Match             5.9%;  Score 113;  DB 14;  Length 318;
  Best Local Similarity   99.4%;  Pred. No. 8.8e-20;
  Matches  163;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1042 CGTGCATTGGAGAGCCCATTATCACCAATCGTGATACTTGCTACAAATAGGGGAATATGT 1101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 CGTGCATTGGAGAGCCCATTATCACCAATCGTGATACTTGCTACAAATAGGGGAATATGT 259

Qy - 1102 AATGTAAGAGGAACTGATATGACAAGTCCACATGGTATACCGGTGGATCTTCTAGATAGG 1161
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    258 AATGTAAGAGGAACTGATATGCCAAGTCCACATGGTATACCGGTGGATCTTCTAGATAGG 199

Qy   1162 CTGGTGATTATTCGGACAGAGACATATGGCCCTACTGAGATGAT 1205
           |||||||||||||||||||||||||||||||||||||||||||
Db    198 CTGGTGATTATTCGGACAGAGACATATGGCCCTACTGAGATGAT 155


RESULT 8
BE640273/c
LOCUS       BE640273                375 bp    mRNA    linear   EST 30-AUG-2000
DEFINITION  946082B06.x1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE640273
VERSION     BE640273.1  GI:9953690
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946082  row: B  column: 06.
FEATURES              Location/Qualifiers
     source           1. .375
                      /organism="Zea mays"
                      /cultivar="OH43"
                      /db_xref="taxon:4577"
                      /clone_lib="946 - tassel primordium prepared by Schmidt
                      lab"
                      /tissue_type="tassels"
                      /dev_stage="just after the transition from vegetative to
                      inflorescence development"
                      /lab_host="XLOLR"
                      /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                      Site_2: XhoI; George Chuck dissected immature tassels
                      between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                      library in HybriZAP.  Sample insert size  range was 350 bp
                      to 3 Kb with a 1 Kb average."
BASE COUNT      106 a    106 c     79 g     84 t
ORIGIN

  Query Match             5.8%;  Score 110;  DB 10;  Length 375;
  Best Local Similarity   99.4%;  Pred. No. 4.4e-19;
  Matches  160;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1366 TGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTTGGATGCCAAATCCTCGGCTCGG 1425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTTGGATGCCAAATCCTCGGCTCGG 305

Qy   1426 CTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTTGGATCTCCTGTCGTGGAAGT 1485
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    304 CTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTTGGATCACCTGTCGTGGAAGT 245

Qy   1486 CTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTAGTG 1526
           |||||||||||||||||||||||||||||||||||||||||
Db    244 CTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTAGTG 204


RESULT 9
BG316941/c
LOCUS       BG316941                109 bp    mRNA    linear   EST 26-FEB-2001
DEFINITION  947024C05.x2 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
            sequence.
ACCESSION   BG316941
VERSION     BG316941.1  GI:13126371
KEYWORDS    EST.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 109)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 947024  row: C  column: 05.
FEATURES              Location/Qualifiers
     source           1. .109
                      /organism="Zea mays"
                      /cultivar="B73"
                      /db_xref="taxon:4577"
                      /clone_lib="947 - 2 week shoot from Barkan lab"
                      /tissue_type="leaf and stem, including leaf base"
                      /dev_stage="2 week old seedling (3 leaves)"
                      /lab_host="XL1-Blue"
                      /note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);
```

Site_1: EcoRI; Site_2: XhoI; Directionally cloned using Stratagene's UniZap XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10e5 independent recombinant phage. The plants were greenhouse grown."

BASE COUNT 30 a 29 c 17 g 33 t
ORIGIN

Query Match 5.7%; Score 109; DB 12; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1214 TGGCTATCCGAGCACAAGTGGAGGAGATTGATATGGATGAAGAAAGTCTTGCTTATTTAG 1273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 TGGCTATCCGAGCACAAGTGGAGGAGATTGATATGGATGAAGAAAGTCTTGCTTATTTAG 50

Qy   1274 GCGAGATCGGACAGCAGACATCTTTGAGACATGCTATTCAATTGATATC 1322
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db     49 GCGAGATCGGACAGCAGACATCTTTGAGACATGCTATTCAATTGATATC 1
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Search completed: December 5, 2002, 07:53:46
Job time : 2058 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 06:20:01 ; Search time 73 Seconds
(without alignments)
10213.033 Million cell updates/sec

Title: US-09-589-510-3
Perfect score: 1912
Sequence: 1 acccacgcgtccgcaaattt.....aaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 350425 seqs, 194966369 residues

Word size : 100

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: December 5, 2002, 07:55:17
Job time : 76 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 04:53:19 ; Search time 66 Seconds
(without alignments)
8884.333 Million cell updates/sec

Title: US-09-589-510-3
Perfect score: 1912
Sequence: 1 acccacgcgtccgcaaattt.....aaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 100

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: December 5, 2002, 06:21:18
Job time : 71 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 04:52:00 ; Search time 283 Seconds
(without alignments)
15214.914 Million cell updates/sec

Title: US-09-589-510-3
Perfect score: 1912
Sequence: 1 acccacgcgtccgcaaattt.....aaaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 100

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1912	100.0	1912	22	AAD02567	Maize RuvB ortholo
2	1080	56.5	1869	22	AAD02570	Maize RuvB ortholo
3	576	30.1	1845	22	AAD02566	Maize RuvB ortholo

ALIGNMENTS

RESULT 1

AAD02567
ID AAD02567 standard; cDNA; 1912 BP.
XX
AC AAD02567;
XX
DT 02-MAY-2001 (first entry)
XX
DE Maize RuvB orthologue #2 cDNA.
XX
KW Maize; RuvB orthologue; branch migration; heteroduplex extension;
KW homologous recombination; transformation; transgenic plant; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 94..1461
FT /*tag= a
FT /product= "Maize RuvB orthologue protein #2"
XX
PN WO200105975-A1.
XX
PD 25-JAN-2001.
XX
PF 13-JUN-2000; 2000WO-US16271.
XX
PR 16-JUL-1999; 99US-0144112.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Mahajan PB;
XX
DR WPI; 2001-159537/16.
DR P-PSDB; AAY72563.
XX
PT Novel maize RuvB nucleic acid useful for modulating levels of maize
PT RuvB in plants, as probes or amplification primers in the detection,
PT quantitation or isolation of gene transcripts -
XX
PS Claim 1; Page 70-72; 87pp; English.
XX
CC The present sequence is a Zea mays RuvB orthologue #2 cDNA. RuvB along
CC with RuvA catalyses the branch migration process, also known as
CC heteroduplex extension, in homologous recombination. RuvB is used for
CC the control of homologous recombination or transformation efficiency in
CC transgenic plants. The RuvB nucleotide may be used as probes or
CC amplification primers for detecting, quantifying or isolating gene
CC transcripts, in detecting deficiencies in the mRNA level during screening
CC for desired transgenic plants, for detecting gene mutations, for
CC monitoring upregulation of expression or changes in enzyme activity, for
CC detecting any number of allelic variants, orthologues or paralogues of
CC the gene, or for site directed mutagenesis in eukaryotic cells. It may
CC also be used for recombinant expression of its encoded polypeptide, or
CC for use as immunogen in preparing and/or screening of antibodies, and in
CC sense or antisense suppression of one or more genes in a host cell,
CC tissue or plant. The RuvB proteins may be used in assays to agonise or
CC antagonise the enzyme function, or as immunogens or antigens for
CC screening antibodies.
XX
SQ Sequence 1912 BP; 547 A; 385 C; 515 G; 462 T; 3 other;

Query Match 100.0%; Score 1912; DB 22; Length 1912;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ACCCACGCGTCCGCAAATTTGTTGCGGCGGGAGAGCCGGAGAGGAGGCAGCTCCACAGAA 60
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Db      1 ACCCACGCGTCCGCAAATTTGTTGCGGCGGGAGAGCCGGAGAGGAGGCAGCTCCACAGAA 60

Qy     61 ACAGAGAGCGCATAACCGGCGGCGTTGGCGGCGATGAGGATCGAGGAGGTGCAGTCGACC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGAGAGCGCATAACCGGCGGCGTTGGCGGCGATGAGGATCGAGGAGGTGCAGTCGACC 120

Qy    121 TCGAAGAAGCAGCGCATCGCCACCCACACCCACATCAAGGGACTCGGCCTCGACGCCAAT 180
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Db    121 TCGAAGAAGCAGCGCATCGCCACCCACACCCACATCAAGGGACTCGGCCTCGACGCCAAT 180

Qy    181 GGGATGGCGATTGCGTTGGCGGCGGGGTTCGTGGGCCAGGCGGCGGCGCGCGAGGCGGCC 240
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Qy    241 GGGCTGGCGGTCGACATGATTCGCCAGAAGAAGATGGCCGGCCGCGCGGTGCTCCTTGCG 300
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Qy    421 GAGGTGCTGATGGAAAATTTCCGTAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    481 GTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGA 540
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Db    481 GTTTATGAAGGAGAGGTTACTGAACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGA 540

Qy    541 TATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAA 600
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Db    541 TATGCAAAAAGCATTAGCCATGTAATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAA 600

Qy    601 CTGAAGTTAGATTCTTCAATTTATGATGCTCTGATCAAGGAAAAGGTGGCAGTGGGTGAT 660
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Qy    721 GCTACAGAATACGATCTTGAAGCTGAAGAGTATGTTCCTATCCCCAAAGGTGAAGTCCAT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GCTACAGAATACGATCTTGAAGCTGAAGAGTATGTTCCTATCCCCAAAGGTGAAGTCCAT 780

Qy    781 AAGAAAAAAGAAATTGTGCAGGATGTCACACTTCATGACCTTGATGCAGCAAATGCTCAG 840
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Qy    841 CCACAAGGTGGCCAAGATATTTTGTCCCTTATGGGCCAGATGATGAAACCACGAAAGACT 900
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Db    841 CCACAAGGTGGCCAAGATATTTTGTCCCTTATGGGCCAGATGATGAAACCACGAAAGACT 900

Qy    901 GAAATCACCGAAAAACTACGCCAAGAAATTAATAAGGTGGTAAATAGATATATCGATGAA 960
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Qy    961 GGAATTGCAGAGCTTGTACCTGGTGTTTTGTTCATTGATGAGGTCCACATGTTGGATATC 1020
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Qy   1081 GCTACAAATAGGGGAATATGTAATGTAAGAGGAACTGATATGACAAGTCCACATGGTATA 1140
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Qy   1141 CCGGTGGATCTTCTAGATAGGCTGGTGATTATTCGGACAGAGACATATGGCCCTACTGAG 1200
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Db   1141 CCGGTGGATCTTCTAGATAGGCTGGTGATTATTCGGACAGAGACATATGGCCCTACTGAG 1200

Qy   1201 ATGATACAGATATTGGCTATCCGAGCACAAGTGGAGGAGATTGATATGGATGAAGAAAGT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1201 ATGATACAGATATTGGCTATCCGAGCACAAGTGGAGGAGATTGATATGGATGAAGAAAGT 1260

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Qy   1501 GTTGCCAGCTCGAAAGTCATCTAGTGCATTGATCTGCTTCACAGGTTCATAGTCTACTGG 1560
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Qy   1561 TCTTGGAGCGAGCACATTTCGGGGGGAACGGCTTGAATTTTGCAGTGCCTGCTTGTGTTA 1620
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Qy   1681 TTGGTCACCGGTGCAGGAATTGCCGTGTGTGTTTTTATCTTGCTCATCGGTGTCCGGAGT 1740
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Db   1681 TTGGTCACCGGTGCAGGAATTGCCGTGTGTGTTTTTATCTTGCTCATCGGTGTCCGGAGT 1740

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RESULT 2
AAD02570
ID   AAD02570 standard; cDNA; 1869 BP.
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AC   AAD02570;
XX
DT   02-MAY-2001  (first entry)
XX
DE   Maize RuvB orthologue #5 cDNA.
XX
KW   Maize; RuvB orthologue; branch migration; heteroduplex extension;
KW   homologous recombination; transformation; transgenic plant; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             64..1380
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PN   WO200105975-A1.
XX
PD   25-JAN-2001.
XX
PF   13-JUN-2000; 2000WO-US16271.
XX
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PR   16-JUL-1999;   99US-0144112.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Mahajan PB;
XX
DR   WPI; 2001-159537/16.
DR   P-PSDB; AAY72566.
XX
PT   Novel maize RuvB nucleic acid useful for modulating levels of maize
PT   RuvB in plants, as probes or amplification primers in the detection,
PT   quantitation or isolation of gene transcripts -
XX
PS   Claim 1; Page 80-82; 87pp; English.
XX
CC   The present sequence is a Zea mays RuvB orthologue #5 cDNA. RuvB along
CC   with RuvA catalyses the branch migration process, also known as
CC   heteroduplex extension, in homologous recombination. RuvB is used for
CC   the control of homologous recombination or transformation efficiency in
CC   transgenic plants. The RuvB nucleotide may be used as probes or
CC   amplification primers for detecting, quantifying or isolating gene
CC   transcripts, in detecting deficiencies in the mRNA level during screening
CC   for desired transgenic plants, for detecting gene mutations, for
CC   monitoring upregulation of expression or changes in enzyme activity, for
CC   detecting any number of allelic variants, orthologues or paralogues of
CC   the gene, or for site directed mutagenesis in eukaryotic cells. It may
CC   also be used for recombinant expression of its encoded polypeptide, or
CC   for use as immunogen in preparing and/or screening of antibodies, and in
CC   sense or antisense suppression of one or more genes in a host cell,
CC   tissue or plant. The RuvB proteins may be used in assays to agonise or
CC   antagonise the enzyme function, or as immunogens or antigens for
CC   screening antibodies.
XX
SQ   Sequence 1869 BP; 539 A; 373 C; 486 G; 471 T; 0 other;
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Query Match 56.5%; Score 1080; DB 22; Length 1869;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   577 AAGACTGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATC 636
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Qy   637 AAGGAAAAGGTGGCAGTGGGTGATGTTATATACATCGAAGCAAATAGTGGAGCAGTGAAA 696
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   556 AAGGAAAAGGTGGCAGTGGGTGATGTTATATACATCGAAGCAAATAGTGGAGCAGTGAAA 615

Qy   697 AGAGTTGGTAGATGTGATTCTTTTGCTACAGAATACGATCTTGAAGCTGAAGAGTATGTT 756
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   616 AGAGTTGGTAGATGTGATTCTTTTGCTACAGAATACGATCTTGAAGCTGAAGAGTATGTT 675

Qy   757 CCTATCCCCAAAGGTGAAGTCCATAAGAAAAAAGAAATTGTGCAGGATGTCACACTTCAT 816
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   817 GACCTTGATGCAGCAAATGCTCAGCCACAAGGTGGCCAAGATATTTTGTCCCTTATGGGC 876
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Db   736 GACCTTGATGCAGCAAATGCTCAGCCACAAGGTGGCCAAGATATTTTGTCCCTTATGGGC 795

Qy   877 CAGATGATGAAACCACGAAAGACTGAAATCACCGAAAAACTACGCCAAGAAATTAATAAG 936
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Qy   937 GTGGTAAATAGATATATCGATGAAGGAATTGCAGAGCTTGTACCTGGTGTTTTGTTCATT 996
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Qy   997 GATGAGGTCCACATGTTGGATATCGAATGTTTTTCTTATCTTAACCGTGCATTGGAGAGC 1056
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Db   916 GATGAGGTCCACATGTTGGATATCGAATGTTTTTCTTATCTTAACCGTGCATTGGAGAGC 975

Qy  1057 CCATTATCACCAATCGTGATACTTGCTACAAATAGGGGAATATGTAATGTAAGAGGAACT 1116
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1117 GATATGACAAGTCCACATGGTATACCGGTGGATCTTCTAGATAGGCTGGTGATTATTCGG 1176
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Qy  1177 ACAGAGACATATGGCCCTACTGAGATGATACAGATATTGGCTATCCGAGCACAAGTGGAG 1236
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Qy  1237 GAGATTGATATGGATGAAGAAAGTCTTGCTTATTTAGGCGAGATCGGACAGCAGACATCT 1296
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Qy  1297 TTGAGACATGCTATTCAATTGATATCACCTGCCAGCGTGGTCTCAAAGACTAATGGAAGA 1356
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Qy  1357 GAGAAAATCTGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTTGGATGCCAAATCC 1416
         |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
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Qy  1417 TCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTTGG 1467
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Db  1336 TCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTTGG 1386
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RESULT 3
AAD02566
ID   AAD02566 standard; cDNA; 1845 BP.
XX
AC   AAD02566;
XX
DT   02-MAY-2001  (first entry)
XX
DE   Maize RuvB orthologue #1 cDNA.
XX
KW   Maize; RuvB orthologue; branch migration; heteroduplex extension;
KW   homologous recombination; transformation; transgenic plant; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             85..1452
FT                   /*tag=  a
FT                   /product= "Maize RuvB orthologue protein #1"
XX
PN   WO200105975-A1.
XX
PD   25-JAN-2001.
XX
PF   13-JUN-2000; 2000WO-US16271.
XX
PR   16-JUL-1999;   99US-0144112.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
```

PI Mahajan PB;
XX
DR WPI; 2001-159537/16.
DR P-PSDB; AAY72562.
XX
PT Novel maize RuvB nucleic acid useful for modulating levels of maize
PT RuvB in plants, as probes or amplification primers in the detection,
PT quantitation or isolation of gene transcripts -
XX
PS Claim 1; Page 67-69; 87pp; English.
XX
CC The present sequence is a Zea mays RuvB orthologue #1 cDNA. RuvB along
CC with RuvA catalyses the branch migration process, also known as
CC heteroduplex extension, in homologous recombination. RuvB is used for
CC the control of homologous recombination or transformation efficiency in
CC transgenic plants. The RuvB nucleotide may be used as probes or
CC amplification primers for detecting, quantifying or isolating gene
CC transcripts, in detecting deficiencies in the mRNA level during screening
CC for desired transgenic plants, for detecting gene mutations, for
CC monitoring upregulation of expression or changes in enzyme activity, for
CC detecting any number of allelic variants, orthologues or paralogues of
CC the gene, or for site directed mutagenesis in eukaryotic cells. It may
CC also be used for recombinant expression of its encoded polypeptide, or
CC for use as immunogen in preparing and/or screening of antibodies, and in
CC sense or antisense suppression of one or more genes in a host cell,
CC tissue or plant. The RuvB proteins may be used in assays to agonise or
CC antagonise the enzyme function, or as immunogens or antigens for
CC screening antibodies.
XX
SQ Sequence 1845 BP; 530 A; 378 C; 490 G; 445 T; 2 other;

Query Match 30.1%; Score 576; DB 22; Length 1845;
Best Local Similarity 98.8%; Pred. No. 6.5e-214;
Matches 1426; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     144 CCACACCCACATCAAGGGACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGC 203
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Db     135 CCACACCCACATCAAGGGACTCGGCCTCGACGCCAATGGGATGGCGATTGCGTTGGCGGC 194

Qy     204 GGGGTTCGTGGGCCAGGCGGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCG 263
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     195 GGGGTTCGTGGGCCAGTCGGCGGCGCGCGAGGCGGCCGGGCTGGCGGTCGACATGATTCG 254

Qy     264 CCAGAAGAAGATGGCCGGCCGCGCGGTGCTCCTTGCGGGTCCGCCCGCCACGGGCAAGAC 323
           |||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     255 CCAGAAAAAGATGGCCGGCCGCGCGGTGCTCCTTGTGGGTCCGCCCGCCACGGGCAAGAC 314

Qy     324 GGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGTCCTATGGT 383
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     315 GGCGCTAGCGCTCGGCATAGCCCAGGAGCTCGGCAGCAAGGTCCCTTTCTGCCCTATGGT 374

Qy     384 AGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCG 443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     375 AGGATCAGAAGTGTACTCCTCGGAGGTCAAGAAAACTGAGGTGCTGATGGAAAATTTCCG 434

Qy     444 TAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGA 503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     435 TAGAGCTATAGGTTTGCGTATAAAGGAAAACAAAGAGGTTTATGAAGGAGAGGTTACTGA 494

Qy     504 ACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTAGCCATGT 563
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     495 ACTTTCCCCAGAAGAGGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTAGCCATGT 554

Qy     564 AATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTA 623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     555 AATCATCAGCTTAAAGACTGTTAAAGGGACTAAGCAACTGAAGTTAGATTCTTCAATTTA 614

Qy     624 TGATGCTCTGATCAAGGAAAAGGTGGCAGTGGGTGATGTTATATACATCGAAGCAAATAG 683
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     615 TGATGCTCTGATCAAGGAAAAGGTGGCAGTGGGTGATGTTATATACATTGAAGCAAATAG 674

Qy     684 TGGAGCAGTGAAAAGAGTTGGTAGATGTGATTCTTTTGCTACAGAATACGATCTTGAAGC 743
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     675 TGGAGCAGTGAAAAGAGTTGGTAGATGTGATTCTTTTGCTACAGAATACGATCTTGAAGC 734

Qy     744 TGAAGAGTATGTTCCTATCCCCAAAGGTGAAGTCCATAAGAAAAAAGAAATTGTGCAGGA 803
           |||||| ||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     735 TGAAGAATATGTTCCTATCCCCAAAGGTGAAGTCCATAAGAAAAAAGAAATAGTGCAGGA 794

Qy     804 TGTCACACTTCATGACCTTGATGCAGCAAATGCTCAGCCACAAGGTGGCCAAGATATTTT 863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     795 TGTCACACTTCATGACCTTGATGCAGCAAATGCTCAGCCACAAGGTGGCCAAGATATTTT 854

Qy     864 GTCCCTTATGGGCCAGATGATGAAACCACGAAAGACTGAAATCACCGAAAAACTACGCCA 923
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     855 GTCCCTTATGGGCCAGATGATGAAACCACGAAAGACTGAAATCACCGAAAAACTACGCCA 914

Qy     924 AGAAATTAATAAGGTGGTAAATAGATATATCGATGAAGGAATTGCAGAGCTTGTACCTGG 983
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     915 AGAAATTAATAAGGTGGTAAATAGATATATCGATGAAGGAATTGCAGAGCTTGTACCTGG 974

Qy     984 TGTTTTGTTCATTGATGAGGTCCACATGTTGGATATCGAATGTTTTTCTTATCTTAACCG 1043
           |||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     975 TGTTTTATTCATTGACGAGGTCCACATGTTGGATATCGAATGTTTTTCTTATCTTAACCG 1034

Qy    1044 TGCATTGGAGAGCCCATTATCACCAATCGTGATACTTGCTACAAATAGGGGAATATGTAA 1103
           |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Db    1035 TGCATTGGAGAGCCCATTATCACCAATTGTGATACTTGCTACGAATAGGGGAATATGTAA 1094

Qy    1104 TGTAAGAGGAACTGATATGACAAGTCCACATGGTATACCGGTGGATCTTCTAGATAGGCT 1163
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||
Db    1095 TGTAAGAGGAACTGATATGACAAGTCCACATGGTATACCAGTGGATCTTCTAGATAGGTT 1154

Qy    1164 GGTGATTATTCGGACAGAGACATATGGCCCTACTGAGATGATACAGATATTGGCTATCCG 1223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1155 GGTGATTATTCGGACAGAGACATATGGCCCTACTGAGATGATACAGATATTGGCTATCCG 1214

Qy    1224 AGCACAAGTGGAGGAGATTGATATGGATGAAGAAAGTCTTGCTTATTTAGGCGAGATCGG 1283
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1215 AGCACAAGTGGAGGACATTGATATGGATGAAGAAAGTCTTGCTTATTTAGGCGAGATCGG 1274

Qy    1284 ACAGCAGACATCTTTGAGACATGCTATTCAATTGATATCACCTGCCAGCGTGGTCTCAAA 1343
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1275 ACAGCAGACATCTTTAAGACATGCTATTCAATTGATATCACCTGCCAGCGTGGTCTCAAA 1334

Qy    1344 GACTAATGGAAGAGAGAAAATCTGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTT 1403
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    1335 GACTAATGGAAGAGAGAAAATATGCAAGGCTGATCTCGAGGAAGTCAGTGGGCTCTATTT 1394

Qy    1404 GGATGCCAAATCCTCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGAT 1463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1395 GGATGCCAAATCCTCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGAT 1454

Qy    1464 TTGGATCTCCTGTCGTGGAAGTCTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTA 1523
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1455 TTGGATCACCTGTCGTGGAAGTCTCGAAGAGAATGTAGTTGCCAGCTCGAAAGTCATCTA 1514

Qy    1524 GTG 1526
           |||
Db    1515 GTG 1517
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Search completed: December 5, 2002, 06:19:48
Job time : 289 secs